

FIG. 1A

1	ATCCTTGCTGGAGCATTCACTAGGCGAGGCGCTCCATCGGACTCACTAGCCGCACTCATG	60
1	M	1
61	AATCGGCACCATCTGCAGGATCACTTTCTGGAAATAGACAAGAAGAACTGCTGTGTGTTT	120
2	N R H H L Q D H F L E I D K K N C C V F	21
121	CGAGATGACTTCATTGTCAAGGTGTTGCCGCCGTGTTGGGGCTGGAGTTTATCTTCGGG	180
22	R D D F I V K V L P P V L G L E <u>F I F G</u>	41
181	CTTCTGGGCAATGGCCTTGCCCTGTGGATTTTCTGTTTCCACCTCAAGTCTGGAAATCC	240
42	<u>L L G N G L A L W I F C F</u> H L K S W K S	61
241	AGCCGGATTTTCTGTTC AACCTGGCAGTGGCTGACTTTCTACTGATCATCTGCCTGCCC	300
62	S R <u>I F L F N L A V A D F L L I I C L P</u>	81
301	TTCCTGATGACAACATATGTGAGGCGTTGGGACTGGAAGTTTGGGGACATCCCTTGCCGG	360
82	<u>F L M</u> D N Y V R R W D W K <u>F G D I P C R</u>	101
361	CTGATGCTCTTCATGTTGGCTATGAACGCCAGGGCAGCATCATCTTCCTCACGGTGGTG	420
102	<u>L M L F M L A M N R Q G S I I F L T V V</u>	121
421	GCGGTAGACAGGTATTTCCGGTGGTCCATCCCCACCACGCCCTGAACAAGATCTCCAAT	480
122	<u>A V</u> D R Y F R V V H P H H A L N K I S N	141
481	CGGACAGCAGCCATCATCTCTTGCTTCTGTGGGGCATCACTATTGGCCTGACAGTCCAC	540
142	R T <u>A A I I S C L L W G I T I G L T V H</u>	161
541	CTCCTGAAGAAGAAGATGCCGATCCAGAATGGCGGTGCAAATTTGTGCAGCAGCTTCAGC	600
162	<u>L L</u> K K K M P I Q N G G A N L C S S F S	181
601	ATCTGCCATACCTTCCAGTGGCACGAAGCCATGTTCTCTGGAGTTCTTCTGCCCTG	660
182	I C H T F Q W H E <u>A M F L L E F F L P L</u>	201
661	GGCATCATCTGTTCTGCTCAGCCAGAATTATCTGGAGCCTGCGGCAGAGACAAATGGAC	720
202	<u>G I I L F C S A</u> R I I W S L R Q R Q M D	221
721	CGGCATGCCAAGATCAAGAGAGCCATCACCTTCATCATGGTGGTGGCCATCGTCTTTGTC	780
222	R H A K I K R <u>A I T F I M V V A I V F V</u>	241
781	ATCTGCTTCCTTCCCAGCGTGGTTGTGCGGATCCGCATCTTCTGGCTCCTGCACACTTCG	840
242	<u>I C F L P S V V V</u> R I R I F W L L H T S	261
841	GGCACGCAGAATTGTGAAGTGTACCGCTCGGTGGACCTGGCGTTCTTTTACTCTCAGC	900
262	G T Q N C E V Y R S V D <u>L A F F I T L S</u>	281
901	TTCACCTACATGAACAGCATGCTGGACCCCGTGGTGTACTACTTCTCCAGCCCATCCTTT	960
282	<u>F T Y M N S M L D P V V Y Y F S</u> S P S F	301

FIG. 2A

		1		50							
HGPRBMY74	(1)	MNRHHLQ	DHFL	ETDKKNCCVFRDDFI	IKVLPPVLGLEF	IFGLLGNGLALW					
HM74	(1)	MNRHHLQ	DHFL	ETDKKNCCVFRDDFI	IAKVLPPVLGLEF	IFGLLGNGLALW					
HM74A	(1)	MNRHHLQ	DHFL	ETDKKNCCVFRDDFI	IKVLPPVLGLEF	IFGLLGNGLALW					
Q9EP66	(1)	---MSKS	DHFL	VINGKNCCVFRDENI	IAKVLPPVLGLEF	IFGLLGNGLALW					
GP31_HUMAN	(1)	-----	MPFPNC	SAPSTVVATAVGVTL	LGLECGI	GLLGNAVALW					
Q9NQ20	(1)	-----	MPFPNC	SAPSTVVATAVGVTL	LGLECGI	GLLGNAVALW					
Q9BXC0	(1)	-----	MYNGSC	CRTEGDTISQVMP	PLLIVAFV	LGALNGVALC					
Q9JLS1	(1)	-----	MEHTNC	SAASTVVETAVG	ITMLTECVL	GLMGNAVALW					
		51		100							
HGPRBMY74	(51)	IFCFHLKSWKS	SRIF	ELFNLA	VADFLLI	ICLPFLMDNYVRRWDWKFGDIPC					
HM74	(51)	IFCFHLKSWKS	SRIF	ELFNLA	VADFLLI	ICLPFLMDNYVRRSDWNFGDIPC					
HM74A	(51)	IFCFHLKSWKS	SRIF	ELFNLA	VADFLLI	ICLPFLMDNYVRRWDWKFGDIPC					
Q9EP66	(48)	IFCFHLKSWKS	SRIF	ELFNLA	VADFLLI	ICLPFLTDNYVHNWDWRFGGIPC					
GP31_HUMAN	(38)	TFLFRVRVWK	PYAVY	LLNLAL	ADLLA	ACLPFLAAFYLSQAWHLGRVGC					
Q9NQ20	(38)	TFLFRVRVWK	PYAVY	LLNLAL	ADLLA	ACLPFLAAFYLSQAWHLGRVGC					
Q9BXC0	(39)	GFCFHMKT	WKPE	STVY	LFNLAVADFL	MLICLPERTDYLRRRHWAFGDIPC					
Q9JLS1	(38)	TEFYRLKV	WKPE	PYAVY	LFNLV	VADLLATSVPLAAFYLRGKTWKLGHMPC					
		101		150							
HGPRBMY74	(101)	RLVLFMLAMNRQGSII	FLTVVAVDRY	FRVVHPHHA	LNKISNR	TAAATISCL					
HM74	(101)	RLVLFMLAMNRQGSII	FLTVVAVDRY	FRVVHPHHA	LNKISN	WTAAATISCL					
HM74A	(101)	RLVLFMLAMNRQGSII	FLTVVAVDRY	FRVVHPHHA	LNKISNR	TAAATISCL					
Q9EP66	(98)	RVMLFMLAMNRQGSII	FLTVVAVDRY	FRVVHPH	FLN	KNISNR	TAAATISCF				
GP31_HUMAN	(88)	WALHFL	LDLSR	SVGMAFLAA	VALD	RYLRVVHPR	LKVNLLSPOAALGV				
Q9NQ20	(88)	WALHFL	LDLSR	SVGMAFLAA	VALD	RYLRVVHPR	LKVNLLSPOAALGV				
Q9BXC0	(89)	RVGL	FTLAMNRAGSI	VF	LT	VVAADRYEKVVH	PHAVNTISTRVAAGIVCT				
Q9JLS1	(88)	QLLFL	LALAES	CGVGVAF	ILMTVAL	DRYLHV	VHPRLRVNL	LSLRAAWGISSL			
		151		200							
HGPRBMY74	(151)	LWGL	ITIGLTVHLL	KKKMPI	QNGG--	ANLCSSFS	ICHTFOWHEAMFLLEFF				
HM74	(151)	LWGL	ITVGLTVHLL	KKKLLI	QNGP--	ANVCIS	FSICHTFRWHEAMFLLEFF				
HM74A	(151)	LWGL	ITIGLTVHLL	KKKMPI	QNGG--	ANLCSSFS	ICHTFOWHEAMFLLEFF				
Q9EP66	(148)	LWGL	ITIGLTVHLL	YTNMTK	NGE--	AYLCSSFS	ICYNFRWHDAMFLLEFF				
GP31_HUMAN	(138)	VWLL	LMVALTC	PLLISEAA	QNST	RCHSEY	SRADGSESI	WQEA	LSC	LOFV	
Q9NQ20	(138)	VWLL	LMVALTC	PLLISEAA	QNST	RCHSEY	SRADGSESI	WQEA	LSC	LOFV	
Q9BXC0	(139)	LWAL	VILGT	VYLL	LNHL	CVQET--	AVSC	SEIMES	ANGWHDIM	FOLEFF	
Q9JLS1	(138)	FWLL	LMV	VLTP	QNL	LTCRTT	QNST	ECPS	EYET	GGTKAIATCQEV	LFFLOVL
		201		250							
HGPRBMY74	(199)	LPLGI	IILFCSARI	IWSLRQ	RQ--	MDRHAKIKRAIT	FIMVVAIVF	VICFLP			
HM74	(199)	LPLGI	IILFCSARI	IWSLRQ	RQ--	MDRHAKIKRAIT	FIMVVAIVF	VICFLP			
HM74A	(199)	LPLGI	IILFCSARI	IWSLRQ	RQ--	MDRHAKIKRAIT	FIMVVAIVF	VICFLP			
Q9EP66	(196)	LPLAI	IILFCSARI	IWSLRQ	RQ--	MDRHAKIKRAIN	FIMVVAIVF	VICFLP			
GP31_HUMAN	(188)	LPEGL	IVFCNAGI	IRALOK	RLREPEKOP	KLORAQ	ALVITVVV	L	FAL	CFLP	
Q9NQ20	(188)	LPEGL	IVFCNAGI	IRALOK	RLREPEKOP	KLORAQ	ALVITVVV	L	FAL	CFLP	
Q9BXC0	(187)	MPLGI	IILFCS	FKI	IWSLR	RQ--	LRARQ	ARMKAT	RFIMVVAIVF	ITCYLP	
Q9JLS1	(188)	LPEGL	ISFCNSGL	IRTL	OKRL	SESDKO	PTIRAR	VLVA	MLL	FGLCFLP	

FIG. 2B

		251		300
HGPRBMY74	(247)	SVVRIRIFWLLHTSGTONCEVYRSVDLAFFITLSFTYMNSMLDPVVYYF		
HM74	(247)	SVVRIRIFWLLHTSGTONCEVYRSVDLAFFITLSFTYMNSMLDPVVYYF		
HM74A	(247)	SVVRIRIFWLLHTSGTONCEVYRSVDLAFFITLSFTYMNSMLDPVVYYF		
Q9EP66	(244)	SVVRIRIFWLLYKYNVRNCDIYSVDLAFFITLSFTYMNSMLDPVVYYF		
GP31_HUMAN	(238)	CFLARVLMHIFONLGSCR--ALC-AVAHTSDVTGSLTYLHSSVNPVVYCF		
Q9NQ20	(238)	CFLARVLMHIFONLGSCR--ALC-AVAHTSDVTGSLTYLHSSVNPVVYCF		
Q9BXC0	(236)	SVSARLYFLWTVPSSACD--P---SVHGALHITLSFTYMNSMLDPVVYYF		
Q9JLS1	(238)	SVLRVLMHIFQEFKSCS--VQQ-ATMRASDIAGSLTCLHSTLSPATYCF		
		301		350
HGPRBMY74	(297)	SSPSFPNFEFTLINRCLQRKMTGEPDNNRSTSVELTGDPN-KTRGAPEAL		
HM74	(297)	SSPSFPNFEFTLINRCLQRKMTGEPDNNRSTSVELTGDPN-KTRGAPEAL		
HM74A	(297)	SSPSFPNFEFTLINRCLQRKMTGEPDNNRSTSVELTGDPN-KTRGAPEAL		
Q9EP66	(294)	SSPSFPNFEFTLINRCLQRKMTGEPDNNRSTSVELTGDPN-KTRGAPEAL		
GP31_HUMAN	(285)	SSPTFRSSYRRVFHTLRGKGQAAEPPDFNERDSYS-----		
Q9NQ20	(285)	SSPTFRSSYRRVFHTLRGKGQAAEPPDFNERDSYS-----		
Q9BXC0	(281)	SSPSFPKIFYNKLIKICSLKPKQPGHSKTORPEEMPTSNLGRRCISVANSE		
Q9JLS1	(285)	SNPAFTHSYRKVLKSLRGRRKAAESPSDNLDSYS-----		
		351		392
HGPRBMY74	(346)	MANSGEPWSPSYLCPTSNNHSSKKGHCHQEPASLEKQLGCCIE		
HM74	(346)	MANSGEPWSPSYLCPTSNNHSSKKGHCHQEPASLEKQLGCCIE		
HM74A	(346)	MANSGEPWSPSYLCPTSP-----		
Q9EP66	(343)	MADESEPGSPPYLASTSR-----		
GP31_HUMAN	(320)	-----		
Q9NQ20	(320)	-----		
Q9BXC0	(331)	QSQSDGQWDPHIVEWH-----		
Q9JLS1	(320)	-----		

5/7

FIG. 3

D = PF_ls_8.29 7tm_1 PF00001 7 transmembrane receptor (rhodopsin family)

Identical Match = 62 Similar = 175 Total # Of Gaps = 10

Identity: Alignment = 22% Query = 16% Target = 23%

Similarity: Alignment = 63% Query = 46% Target = 64%

QS = 41 QE = 291 TS = 1 TE = 275

```

Q      41 GNGLALWIFCFHLKSWKSSRIFLFLNLAVADFLLIICLPFLMDNYVRR--WDWKFGDIPCR
      GN+L++W++C+H +   +++ +F++NLAVAD+L+ + +P+ M   Y+   +W FG++ C+
T      1 GNILVIWVICRHKRMRTPTNYFICNLAVADLLFCLTCPWMLYYFHWGHHHPFGRAMCK

Q      99 LMLFMLAMNRQGSIIFLTVAVDYFRVVHPPHALNKIS-NRTAAIISCLLWGITIGLTV
      +  ++  M+   SI FL++ ++DRY  ++HP ++ ++ +  R A+++++ W + + +++
T      61 IWTFYFFYMCCYASIFFLCCISIDRYWAICHPMRYRRRMTRPRHAWVMCLVIWVLAFLWSL

Q     158 HL-LK-KKMPIQNGG-----ANLCSSFSICHT-----FQWHEAMFLEFFLPLGII
      +  +  + +++++   ++ C+ +   ++   +++   +++ F++PL ++
T     121 PPLMFWWCYTHECPNHWNNCNHTWCFIDWPHESSHWWTWWRYYYICSCIVGFYIPLLVM

Q     202 LFCSARIIWSLRQRQM-----DRHAKIKRAITFIMVVAIVFVICFLPSVVVRIRIFWLLH
      +FC RI++ L+++ +   R  K ++A   + VV +VF++C+LP  ++ + +++++
T     181 CFCYCRIYRTLWRHARQMASKMRSRKERKAAKMLCVVVVVFFVCWLPYHIFMF-MDTFC-

Q     257 TSGT--QNCEVYRSVDLAFFITLSFTYMNSMLDPVVY
      ++ +  ++CE+ + ++ A++I++ ++Y N++L+P++Y
T     239 MHWWMCWTCELECVPWAYQICVWLAYVNCCLNPIIY

```

FIG. 4

Protein	Genbank/SWI SS-PROT Accession	Identities	Similarities
Human HM74 Protein	P49019	95.9%	97.2%
Human HM74 Splice Variant Protein, HM74A	gi AAW94654	93.5%	93.5%
Mouse Seven Transmembrane Spanning Receptor Protein	Q9EP66	76.2%	80.1%
Human GPR31 Protein	O00270	26.9%	39.6%
Human GPR31 Variant Protein	Q9NQ20	27.1%	39.6%
Human Chemokine Receptor Protein	Q9BXC0	46.9	58.0%
Mouse G-Protein Coupled Receptor Protein	Q9JLS1	26.5%	39.3%

FIG. 5

BMY74V5His FLIPR

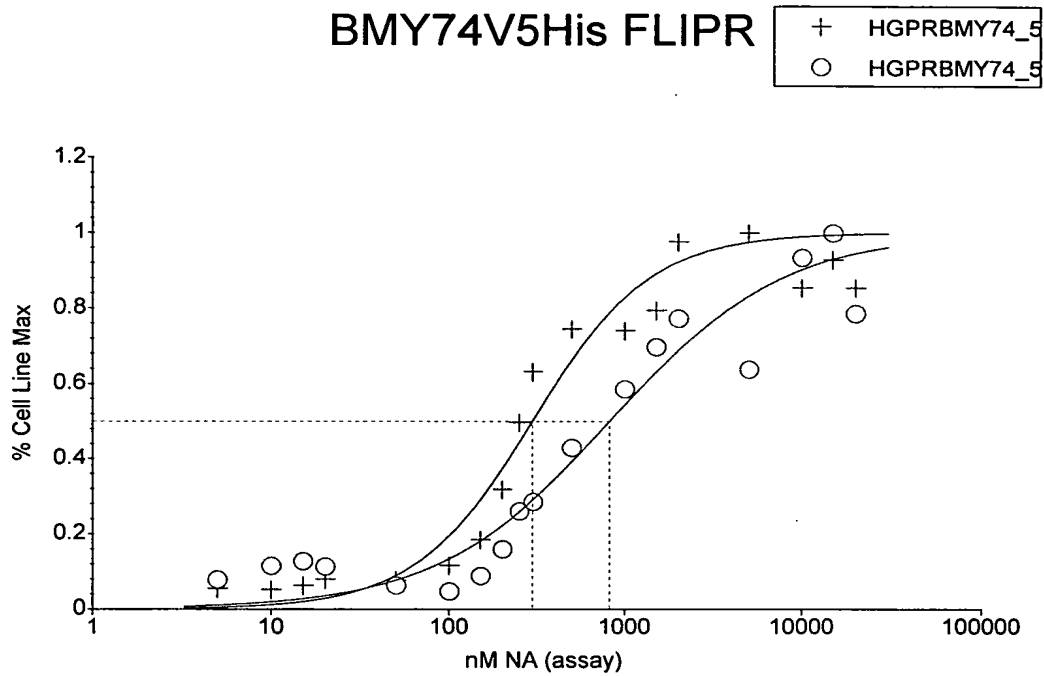


FIG. 6

HM74a vs. HGPRBMY74V5His FLIPR

